

SEQUENZPROTOKOLL

(1) ALLGEMEINE ANGABEN:

(i) ANMELDER:

- (A) NAME: Deutsches Krebsforschungszentrum
- (B) STRASSE: Im Neuenheimer Feld 280
- (C) ORT: Heidelberg
- (E) LAND: Deutschland
- (F) POSTLEITZAHL: 69120
- (G) TELEFON:

(ii) BEZEICHNUNG DER ERFINDUNG: Protein zur Inhibierung von Apoptose

(iii) ANZAHL DER SEQUENZEN: 3

(iv) COMPUTER-LESBARE FASSUNG:

- (A) DATENTRÄGER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) BETRIEBSSYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(v) DATEN DER JETZIGER ANMELDUNG:

ANMELDENUMMER: PCT/DE98/00940

(vi) DATEN DER URANMELDUNG:

- (A) ANMELDENUMMER: DE 197 134 34.3
- (B) ANMELDETAG: 01-APR-1997

(2) ANGABEN ZU SEQ ID NO: 1:

(i) SEQUENZKENNZEICHEN:

- (A) LÄNGE: 313 Basenpaare
- (B) ART: Nucleotid
- (C) STRANGFORM: Einzelstrang
- (D) TOPOLOGIE: nicht bekannt

(ii) ART DES MOLEKÜLS: cDNA

(iii) HYPOTHETISCH: NEIN

(iv) ANTISENSE: NEIN

(ix) MERKMAL:

- (A) NAME/SCHLÜSSEL: CDS
- (B) LAGE: 3..313

(ix) MERKMAL:

- (A) NAME/SCHLÜSSEL: mat_peptide
- (B) LAGE: 3..313

(xi) SEQUENZBESCHREIBUNG: SEQ ID NO: 1:

AG	AGT	AGG	ATG	TCT	GCT	GAA	GTC	ATC	CAT	CAG	GTT	GAA	GAA	GCA	CTT	47
Ser	Arg	Met	Ser	Ala	Glu	Val	Ile	His	Gln	Val	Glu	Glu	Ala	Leu		
1				5					10					15		
GAT	ACA	GAT	GAG	AAG	GAG	ATG	CTG	CTC	TTT	TTG	TGC	CGG	GAT	GTT	GCT	95
Asp	Thr	Asp	Glu	Lys	Glu	Met	Leu	Leu	Phe	Leu	Cys	Arg	Asp	Val	Ala	
			20						25					30		
ATA	GAT	GTG	GTT	CCA	CCT	AAT	GTC	AGG	GAC	CTT	CTG	GAT	ATT	TTA	CGG	143
Ile	Asp	Val	Val	Pro	Pro	Asn	Val	Arg	Asp	Leu	Leu	Asp	Ile	Leu	Arg	
			35					40					45			
GAA	AGA	GGT	AAG	CTG	TCT	GTC	GGG	GAC	TTG	GCT	GAA	CTG	CTC	TAC	AGA	191
Glu	Arg	Gly	Lys	Leu	Ser	Val	Gly	Asp	Leu	Ala	Glu	Leu	Leu	Tyr	Arg	
		50					55					60				
GTG	AGG	CGA	TTT	GAC	CTG	CTC	AAA	CGT	ATC	TTG	AAG	ATG	GAC	AGA	AAA	239
Val	Arg	Arg	Phe	Asp	Leu	Leu	Lys	Arg	Ile	Leu	Lys	Met	Asp	Arg	Lys	
	65					70					75					
GCT	GTG	GAG	ACC	CAC	CTG	CTC	AGG	AAC	CCT	CAC	CTT	GTT	TCG	GAC	TAT	287
Ala	Val	Glu	Thr	His	Leu	Leu	Arg	Asn	Pro	His	Leu	Val	Ser	Asp	Tyr	
	80				85					90					95	
AGA	GTG	CTG	ATG	TCA	GAG	ATT	GGT	GA								313
Arg	Val	Leu	Met	Ser	Glu	Ile	Gly									
				100												

(2) ANGABEN ZU SEQ ID NO: 2:

(i) SEQUENZKENNZEICHEN:

- (A) LÄNGE: 103 Aminosäuren
- (B) ART: Aminosäure
- (D) TOPOLOGIE: linear

(ii) ART DES MOLEKÜLS: Protein

(xi) SEQUENZBESCHREIBUNG: SEQ ID NO: 2:

Ser	Arg	Met	Ser	Ala	Glu	Val	Ile	His	Gln	Val	Glu	Glu	Ala	Leu	Asp
1				5					10					15	
Thr	Asp	Glu	Lys	Glu	Met	Leu	Leu	Phe	Leu	Cys	Arg	Asp	Val	Ala	Ile
			20					25					30		
Asp	Val	Val	Pro	Pro	Asn	Val	Arg	Asp	Leu	Leu	Asp	Ile	Leu	Arg	Glu
			35				40					45			
Arg	Gly	Lys	Leu	Ser	Val	Gly	Asp	Leu	Ala	Glu	Leu	Leu	Tyr	Arg	Val
	50					55					60				

Arg Arg Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala
 65 70 75 80
 Val Glu Thr His Leu Leu Arg Asn Pro His Leu Val Ser Asp Tyr Arg
 85 90 95
 Val Leu Met Ser Glu Ile Gly
 100

(2) ANGABEN ZU SEQ ID NO: 3:

(i) SEQUENZKENNZEICHEN:

- (A) LÄNGE: 1443 Basenpaare
- (B) ART: Nucleotid
- (C) STRANGFORM: Einzelstrang
- (D) TOPOLOGIE: linear

(ii) ART DES MOLEKÜLS: cDNA

(iii) HYPOTHETISCH: NEIN

(iv) ANTISENSE: NEIN

(ix) MERKMAL:

- (A) NAME/SCHLÜSSEL: CDS
- (B) LÄGE: 1..1440

(xi) SEQUENZBESCHREIBUNG: SEQ ID NO: 3:

ATG TCT GCT GAA GTC ATC CAT CAG GTT GAA GAA GCA CTT GAT ACA GAT	48
Met Ser Ala Glu Val Ile His Gln Val Glu Glu Ala Leu Asp Thr Asp	
5 10 15	
CAG AAG GAG ATG CTG CTC TTT TTG TGC CGG GAT GTT GCT ATA GAT GTG	96
Glu Lys Glu Met Leu Leu Phe Leu Cys Arg Asp Val Ala Ile Asp Val	
20 25 30	
GTT CCA CCT AAT GTC AGG GAC CTT CTG GAT ATT TTA CGG GAA AGA GGT	144
Val Pro Pro Asn Val Arg Asp Leu Leu Asp Ile Leu Arg Glu Arg Gly	
35 40 45	
AAG CTG TCT GTC GGG GAC TTG GCT GAA CTG CTC TAC AGA GTG AGG CGA	192
Lys Leu Ser Val Gly Asp Leu Ala Glu Leu Leu Tyr Arg Val Arg Arg	
50 55 60	
TTT GAC CTG CTC AAA CGT ATC TTG AAG ATG GAC AGA AAA GCT GTG GAG	240
Phe Asp Leu Leu Lys Arg Ile Leu Lys Met Asp Arg Lys Ala Val Glu	
65 70 75 80	

ACC Thr	CAC His	CTG Leu	CTC Leu	AGG Arg 85	AAC Asn	CCT Pro	CAC His	CTT Leu	GTT Val 90	TCG Ser	GAC Asp	TAT Tyr	AGA Arg	GTG Val 95	CTG Leu	288
ATG Met	GCA Ala	GAG Glu	ATT Ile 100	GGT Gly	GAG Glu	GAT Asp	TTG Leu	GAT Asp 105	AAA Lys	TCT Ser	GAT Asp	GTG Val	TCC Ser 110	TCA Ser	TTA Leu	336
ATT Ile	TTC Phe	CTC Leu 115	ATG Met	AAG Lys	GAT Asp	TAC Tyr	ATG Met 120	GGC Gly	CGA Arg	GGC Gly	AAG Lys	ATA Ile 125	AGC Ser	AAG Lys	GAG Glu	384
AAG Lys	AGT Ser 130	TTC Phe	TTG Leu	GAC Asp	CTT Leu	GTG Val 135	GTT Val	GAG Glu	TTG Leu	GAG Glu	AAA Lys 140	CTA Leu	AAT Asn	CTG Leu	GTT Val	432
GCC Ala 145	CCA Pro	GAT Asp	CAA Gln	CTG Leu	GAT Asp 150	TTA Leu	TTA Leu	GAA Glu	AAA Lys	TGC Cys 155	CTA Leu	AAG Lys	AAC Asn	ATC Ile	CAC His 160	480
AGA Arg	ATA Ile	GAC Asp	CTG Leu	AAG Lys 165	ACA Thr	AAA Lys	ATC Ile	CAG Gln	AAG Lys 170	TAC Tyr	AAG Lys	CAG Gln	TCT Ser	GTT Val 175	CAA Gln	528
GGA Gly	GCA Ala	GGG Gly	ACA Thr 180	AGT Ser	TAC Tyr	AGG Arg	AAT Asn	GTT Val 185	CTC Leu	CAA Gln	GCA Ala	GCA Ala	ATC Ile 190	CAA Gln	AAG Lys	576
AGT Ser	CTC Leu	AAG Lys 195	GAT Asp	CCT Pro	TCA Ser	AAT Asn	AAC Asn 200	TTC Phe	AGG Arg	CTC Leu	CAT His	AAT Asn 205	GGG Gly	AGA Arg	AGT Ser	624
GAA Lys 210	GAA Glu	CAA Gln	AGA Arg	CTT Leu	AAG Lys	GAA Glu 215	CAG Gln	CTT Leu	GGC Gly	GCT Ala	CAA Gln 220	CAA Gln	GAA Glu	CCA Pro	GTG Val	672
AAG Lys 225	AAA Lys	TCC Ser	ATT Ile	CAG Gln	GAA Glu 230	TCA Ser	GAA Glu	GCT Ala	TTT Phe	TTG Leu 235	CCT Pro	CAG Gln	AGC Ser	ATA Ile	CCT Pro 240	720
GAA Glu	GAG Glu	AGA Arg	TAC Tyr	AAG Lys 245	ATG Met	AAG Lys	AGC Ser	AAG Lys	CCC Pro 250	CTA Leu	GGA Gly	ATC Ile	TGC Cys	CTG Leu 255	ATA Ile	768
ATC Ile	GAT Asp	TGC Cys	ATT Ile 260	GGC Gly	AAT Asn	GAG Glu	ACA Thr	GAG Glu 265	CTT Leu	CTT Leu	CGA Arg	GAC Asp	ACC Thr 270	TTC Phe	ACT Thr	816

TCC Ser	CTG Leu	GGC Gly 275	TAT Tyr	GAA Glu	GTC Val	CAG Gln	AAA Lys 280	TTC Phe	TTG Leu	CAT His	CTC Leu	AGT Ser 285	ATG Met	CAT His	GGT Gly	864
ATA Ile	TCC Ser 290	CAG Gln	ATT Ile	CTT Leu	GGC Gly	CAA Gln 295	TTT Phe	GCC Ala	TGT Cys	ATG Met	CCC Pro 300	GAG Glu	CAC His	CGA Arg	GAC Asp	912
TAC Tyr 305	GAC Asp	AGC Ser	TTT Phe	GTG Val	TGT Cys 310	GTC Val	CTG Leu	GTG Val	AGC Ser	CGA Arg 315	GGA Gly	GGC Gly	TCC Ser	CAG Gln	AGT Ser 320	960
GTG Val 320	TAT Tyr	GGT Gly	GTG Val	GAT Asp 325	CAG Gln	ACT Thr	CAC His	TCA Ser	GGG Gly 330	CTC Leu	CCC Pro	CTG Leu	CAT His	CAC His 335	ATC Ile	1008
AGG Arg	AGG Arg	ATG Met	TTC Phe 340	ATG Met	GGA Gly	GAT Asp	TCA Ser	TGC Cys 345	CCT Pro	TAT Tyr	CTA Leu	GCA Ala	GGG Gly 350	AAG Lys	CCA Pro	1056
AAG Lys	ATG Met	TTT Phe 355	TTT Phe	ATT Ile	CAG Gln	AAC Asn	TAT Tyr 360	GTG Val	GTG Val	TCA Ser	GAG Glu	GGC Gly 365	CAG Gln	CTG Leu	GAG Glu	1104
GAC Asp	AGC Ser 370	AGC Ser	CTC Leu	TTG Leu	GAG Glu	GTG Val 375	GAT Asp	GGG Gly	CCA Pro	GCG Ala	ATG Met 380	AAG Lys	AAT Asn	GTG Val	GAA Glu	1152
TTC Phe 385	AAG Lys	GCT Ala	CAG Gln	AAG Lys	CGA Arg 390	GGG Gly	CTG Leu	TGC Cys	ACA Thr	GTT Val 395	CAC His	CGA Arg	GAA Glu	GCT Ala	GAC Asp 400	1200
TTC Phe	TTC Phe	TGG Trp	AGC Ser	CTG Leu 405	TGT Cys	ACT Thr	GCG Ala	GAC Asp	ATG Met 410	TCC Ser	CTG Leu	CTG Leu	GAG Glu	CAG Gln 415	TCT Ser	1248
CAC His	AGC Ser	TCA Ser	CCA Pro 420	TCC Ser	CTG Leu	TAC Tyr	CTG Leu 425	CAG Gln	TGC Cys	CTC Leu	TCC Ser	CAG Gln	AAA Lys 430	CTG Leu	AGA Arg	1296
CAA Gln	GAA Glu	AGA Arg 435	AAA Lys	CGC Arg	CCA Pro	CTC Leu	CTG Leu 440	GAT Asp	CTT Leu	CAC His	ATT Ile	GAA Glu 445	CTC Leu	AAT Asn	GGC Gly	1344

GTC	TGG	CTG	CAG	CAC	ACT	CTG	AGA	AAG	AAA	CTT	ATC	CTC	TCC	TAC	ACA	1440
Val	Trp	Leu	Gln	His	Thr	Leu	Arg	Lys	Lys	Leu	Ile	Leu	Ser	Tyr	Thr	
465					470					475					480	

TAA 1443